

SEQUENCE LISTING

<110> Shi, Jinrui
 Beach, Larry
 Wang, Hongyu
 Rafalski, Antoni J.
 Rebecca E. Cahoon

<120> Novel Inositol Polyphosphate Kinase
 Genes and Uses Thereof

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<151> 2001-01-12

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Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro Ser *	
275 280 285	
g	923
<210> 6	
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2060707-4632400T

<213> Zea mays

<400> 6

Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
1 5 10 15
Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
20 25 30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
85 90 95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
100 105 110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
115 120 125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
130 135 140
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145 150 155 160
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
165 170 175
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val
180 185 190
Tyr Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
195 200 205
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
210 215 220
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly
225 230 235 240
Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
245 250 255
Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
260 265 270
Val Ser Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro
275 280 285
Ser

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<211> 1344

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (52)...(921)

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gcacgagggtc agtccgtcac ccctcgccgc catagtcccc ttccccatac c atg tcc
Met Ser
1

57

gac ctc cac ccg ccg gag cac caa gtc gcc ggc cac cgc gcc tcc gcc

105

20060707-116824000T

Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala	5	10	15	
agc aag ctg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg				153
Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro				
20	25	30		
ctc cag gcc ggc gac cgt ggg gag cac gag gtc gcc ttc tat gag gcg				201
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala				
35	40	45	50	
ttc tcc gcc cac gcc gtc ccg gcc cgc atc cga gac acc ttc ttc				249
Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe				
55	60	65		
ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg				297
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly				
70	75	80		
gag ccg cat ctc cac gtc ctc gac gac ctc ctc gcg ggg ttt cag				345
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Gln				
85	90	95		
gcg ccc tgc gca gac atc aag atc ggc gcc atc acg tgg cca ccg				393
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro				
100	105	110		
agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc aag gac ccg ggg				441
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp Arg Gly				
115	120	125	130	
acc acg agc gtt ctc ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc				489
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val				
135	140	145		
ggc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc				537
Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala				
150	155	160		
atg gac acc gcc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc				585
Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser				
165	170	175		
gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gtc tac gga				633
Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly				
180	185	190		
gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc				681
Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe				
195	200	205	210	
gag gag cag act ctg ttc cac ttc tac tcc ggc tcc att ctt ctg ggc				729
Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly				
215	220	225		
tat gat gct gct gca gca ggc gga gat ggg ggt gtc acg				777
Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Val Thr				
230	235	240		

2060707-16824007

gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att	825
Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile	
245 250 255	

gac cac aac ttc ctg ggc ggg ctc tgc tcg atc aag ttc gtt tct	873
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser	
260 265 270	

gac att gtt ccg gag act cct cat acg cag cct ttg ggt cct tct taa	921
Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser *	
275 280 285	

gagaggatcc tggcatttcg atttgataac aaagccctac aagttttgtc tggaaaaaga	981
agcgcctccg aagttgtcg ggtgtggaa tctgagacgg tcgtcgcccc accttgggtgc	1041
cttgccttc cttgcctcg aaacatacgg caaactgc tc tttttcgc aacccctac	1101
ttccgaagaa actttttttt tcccaacttg ggggttcgtatcggttgcgt ctggttgtg	1161
ccatcgctc agagggtgtaa agcatggagg gagggcgttgcgttgcgttgcgttgcgt	1221
cttgcgttc cttgcgttc ctgcgtgttgcgttgcgttgcgttgcgttgcgttgcgttgcgt	1281
gatcgtatgt atggacgttc ctaccccaa acgaatccgt ccgataaaaa aaaaaaaaaaa	1341
aaa	1344

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 <213> Zea mays

<400> 8	
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20 25 30	
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr	
35 40 45	
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr	
50 55 60	
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln	
65 70 75 80	
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly	
85 90 95	
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp	
100 105 110	
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp	
115 120 125	
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg	
130 135 140	
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val	
145 150 155 160	
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val	
165 170 175	
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val	
180 185 190	
Tyr Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala	
195 200 205	
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu	
210 215 220	
Leu Gly Tyr Asp Ala Ala Ala Val Ala Gly Gly Asp Gly Gly Gly	
225 230 235 240	

Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
 245 250 255
 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
 260 265 270
 Val Ser Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro
 275 280 285
 Ser

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 <212> DNA
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gcc aag gac gga atc ctg ggc cca ctc gtc gac gat ttt gga aaa ttc Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe 15 20 25	98
tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc ggc tcc acc Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr 30 35 40 45	146
gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc cac gac tac tcc Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser 50 55 60	194
atc cgc tcc ttc tcc ccc gcc ttt cac ggc acc cgc ctc ctg gac gcc Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala 65 70 75	242
tcc gac ggc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Asp Leu Leu 80 85 90	290
tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg 95 100 105	338
acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys 110 115 120 125	386
aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tcg gga Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly 130 135 140	434
gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln 10	482

206070-4682400T

145

150

155

tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc	530
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser	
160 165 170	
tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca	578
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala	
175 180 185	
acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac	626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp	
190 195 200 205	
tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt	674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu	
210 215 220	
gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg	722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu	
225 230 235	
gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att	770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile	
240 245 250	
gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag	818
Asp His Asn Phe Leu Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys	
255 260 265	
gat atc cta gca gta gca tgt ctt cac aag tga ctgatttca tcgagttaat	871
Asp Ile Leu Ala Val Ala Cys Leu His Lys *	
270 275	
cttatttctta tcagaaaata attatgcttg aattatgttc gcagactaaac tgtttgaagt	931
actgtcgaaa acaaaaataat aatatggact gagaggcaat cttgttctgc taaactccct	991
ttcaagtgc tgcagatac tagcgcgtccc ttcccttt tcatattctg tcaaagtgag	1051
tcatttaata ataataacaa tgcccttcaa ctccaaaaaaa aaaaaaaaaaaa aaaa	1105
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1 5 10 15	
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro	
20 25 30	
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser	
35 40 45	
Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser	
50 55 60	
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly	
65 70 75 80	
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr	
85 90 95	
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His	

2060101-116824001

100	105	110													
Leu	Gly	Asp	Ser	Glu	Asp	Tyr	Ile	Cys	Lys	Cys	Leu	Lys	Lys	Asp	Arg
115	120	125													
Glu	Ser	Ser	Ser	Leu	Pro	Leu	Gly	Phe	Arg	Ile	Ser	Gly	Val	Lys	Asp
130	135	140													
Ser	Ile	Ser	Ser	Trp	Glu	Pro	Thr	Arg	Lys	Ser	Leu	Gln	Cys	Leu	Ser
145	150	155	160												
Ala	His	Gly	Val	Ala	Leu	Val	Leu	Asn	Lys	Phe	Val	Ser	Ser	Asn	Asn
165	170	175													
Ile	Asn	His	Asp	Asp	His	His	Pro	Asp	Cys	Ala	Phe	Ala	Thr	Glu	Val
180	185	190													
Tyr	Gly	Ala	Val	Leu	Glu	Arg	Leu	Gln	Lys	Leu	Lys	Asp	Trp	Phe	Glu
195	200	205													
Val	Gln	Thr	Val	Tyr	His	Phe	Tyr	Ser	Cys	Ser	Val	Leu	Val	Val	Tyr
210	215	220													
Glu	Lys	Asp	Leu	Gly	Lys	Gly	Lys	Ala	Thr	Asn	Pro	Leu	Val	Lys	Leu
225	230	235	240												
Val	Asp	Phe	Ala	His	Val	Val	Asp	Gly	Asn	Gly	Val	Ile	Asp	His	Asn
245	250	255													
Phe	Leu	Gly	Leu	Cys	Ser	Phe	Ile	Lys	Phe	Leu	Lys	Asp	Ile	Leu	
260	265	270													
Ala	Val	Ala	Cys	Leu	His	Lys									
275															

<210> 11
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 <212> DNA
 <213> Eucalyptus grandis

<220>
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5	Met														
10	1														
15															
ctc aag gtc ccg gat cat caa gtc gcc ggt cac cgg gga gac ggg gga	166														
Leu	Lys	Val	Pro	Asp	His	Gln	Val	Ala	Gly	His	Arg	Gly	Gly		
20	25	30													
5	10	15													
aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc	214														
Lys	Leu	Gly	Pro	Leu	Val	Asp	Asp	Ser	Gly	Arg	Phe	Tyr	Lys	Pro	Leu
25	30														
35	40	45													
cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc	262														
Gln	Ser	Asp	His	Arg	Gly	Asp	Thr	Glu	Val	Ala	Phe	Tyr	Glu	Ser	Phe
40	45														
tat tcc aat acc gag atc cca ggt cac att cgc aat ttc ttt cct gcg	310														
Tyr	Ser	Asn	Thr	Glu	Ile	Pro	Gly	His	Ile	Arg	Lys	Phe	Phe	Pro	Ala
50	55	60	65												
ttt cac gga act aag act att gag gcg tct gat gga tcg ggt cct caa	358														
Phe	His	Gly	Thr	Lys	Thr	Ile	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Pro	Gln

206070 "416824h000T

	70	75	80	
cct cac ctg gtt ctg gag gat ctc gtc tecg ggt cgc acg aac cca tct				406
Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser				
85	90	95		
ctc atg gac atc aag act gga tcc aga aca tgg tat ccg gag gcc tct				454
Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser				
100	105	110		
gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc				502
Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser				
115	120	125		
gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc				550
Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser				
130	135	140	145	
gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat				598
Glu Ala Gly Phe Trp Gln Pro Glu Lys Val Val Tyr Ser Phe Asn				
150	155	160		
gcg gac ggt gtc agg tecg gct ctg agg aag aag gtt gtt tat tcc aac ttg				646
Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu				
165	170	175		
tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt				694
Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val				
180	185	190		
tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa				742
Tyr Cys His Arg Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu				
195	200	205		
tgg ttg gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att				790
Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile				
210	215	220	225	
atc tta tat gac agg gag tct gtc ttg gac ggc tgt gca cac ccg aaa				838
Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys				
230	235	240		
gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc				886
Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile				
245	250	255		
gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttg ata cgt				934
Asp His Asn Phe Leu Gly Ile Leu Cys Ser Val Ile Lys Phe Ile Arg				
260	265	270		
gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt				982
Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu				
275	280	285		
gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt				1030
Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Thr Glu Pro Glu Leu				
290	295	300	305	

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca
 Asp His Glu Ala Cys * 310

 ttcttcgcatt cctgtctga caagtgggtc agaatgggtta taataacagt ctattttagt
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 1138
 1195

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 <212> PRT
 <213> Eucalyptus grandis

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 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly
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 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser
 35 40 45
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro
 50 55 60
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro
 65 70 75 80
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro
 85 90 95
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala
 100 105 110
 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr
 115 120 125
 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn
 130 135 140
 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe
 145 150 155 160
 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn
 165 170 175
 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys
 180 185 190
 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys
 195 200 205
 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu
 210 215 220
 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro
 225 230 235 240
 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val
 245 250 255
 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile
 260 265 270
 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn
 275 280 285
 Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu
 290 295 300
 Leu Asp His Glu Ala Cys
 305 310

<210> 13
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<212> DNA

206000-46824001

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21)...(908)

<400> 13

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1 5 10	

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc	101
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly	
15 20 25	

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta	149
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val	
30 35 40	

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata	197
Ala Phe Tyr Glu Ser Phe Ser Asn Asn Ile Pro Glu His Ile	
45 50 55	

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc	245
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser	
60 65 70 75	

act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct	293
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala	
80 85 90	

cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg	341
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp	
95 100 105	

gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat	389
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp	
110 115 120	

agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa	437
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln	
125 130 135	

gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac	485
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr	
140 145 150 155	

atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt	533
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe	
160 165 170	

gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc	581
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly	
175 180 185	

ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata	629
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile	
190 195 200	

206070-1498240074

tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile 205 210 215	677
tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Glu Lys Arg Leu 220 225 230 235	725
gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe 240 245 250	773
gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly 255 260 265	821
ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr 270 275 280	869
aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactcttcc Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu *285 290 295	918
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	1020
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205010-16824000T

Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met
195 200 205
Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala
210 215 220
Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala
225 230 235 240
Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp
245 250 255
Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Leu Cys Ser Leu
260 265 270
Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly
275 280 285
Thr Asn Gly Gln Val Glu Leu
290 295

<210> 15
<211> 899
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (89)...(424)

<400> 15
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Met Pro Asp Leu His Pro Pro Glu
1 5

cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160
His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu
10 15 20

atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208
Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg
25 30 35 40

ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256
Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala
45 50 55

gtc ccg gcc cgc atc cga gac acc ttc ttc ccc cgg ttc cac ggc acg 304
Val Pro Ala Arg Ile Arg Asp Thr Phe Pro Arg Phe His Gly Thr
60 65 70

cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352
Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu
75 80 85

gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400
Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp
90 95 100

atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454
Ile Lys Ile Gly Ala Ile Thr *
105 110

20060101-416824007

coggcgtccg	agtgtcgcc	cccgaggcg	ccgtgtggcg	gacggagcgc	cctgaggta	514
aggctatgg	cattgtcgcc	gtccggcg	tgctccggcg	ctgcgtgtca	tcgcgttgc	574
ggcggaggga	tggaactgccc	gtctcgccgc	gcccgttacg	gaggaaaagg	tggagtcttg	634
tcacacgtgc	gcgagctcaa	ggcggttgc	gagggcaga	ctctgttca	cttctactcg	694
gctgtcgatc	ttctgggtca	tgatgtcgct	gcagtcgcag	caggcggagg	tggggggtg	754
gttaacagtga	agctgggtga	ccttgcacat	gtggccagg	tgatgggtt	gattgaccac	814
aaccttcgtt	gccccgtctg	ctatgtatc	aagtgggtt	ctgacatgtt	tccagagact	874
ccttacacgc	agcaaggcg	aattc				899

<210> 16
<211> 111
<212> PRT
<213> Zea mays

<400> 16						
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Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr						
20	25	30				
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr						
35	40	45				
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr						
50	55	60				
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln						
65	70	75	80			
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly						
85	90	95				
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr						
100	105	110				

<210> 17
<211> 643
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

<400> 17						
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cgcacccatca	cccgccggag	caccaatcg	ccggtcaccc	ccgcctccgg	agcaagctgg	180
gccccgtcat	cgacgggtcc	ggccctttat	acaaggccgt	ccagccggc	gaccgtgggg	240
agcacacgt	cgcccttat	gaggcggt	ccggccaccc	cgccgtcccg	gcccgcattcc	300
gagacaccc	cttcccccccg	ttccacggca	ccggacttct	ccccacccgg	ggccgcacccg	360
ggggacccgc	tcggcactc	gtccctcgacg	accttctcg	gggggtttag	ggcccccgtgc	420
tcgcacat	caagatggc	gccccatcg	ggccacccgg	ttccggcgag	ccctacatcg	480
ncaagtacct	ngccaaggac	cgccggacca	cgagcttct	gtccggatc	cgccgttgc	540
gtccggatcg	tcggcccg	ggccggcg	tggccgacgg	agccggcccg	gggtgaangc	600
tatggacac	cgtccggnc	cgccggntgc	tccggngtgc	a		643

<210> 18
<211> 519
<212> DNA

2000-16824001

<213> Zea mays		
<220>		
<221> misc_feature		
<222> (1)...(519)		
<223> n = A,T,C or G		
<400> 18		
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ggcagactt gtccacttc tactcggcgt cgattcttct gggctatgtat gctgtcgag	120	
tcgcagcagg cggangtggg ggtgggttaa cagtgaactt ggtggactttt gcccatgtgg	180	
ccgagggtga tgggggtattt gaccacaactt tccctggcgg gctctgtctan ctgatcaagt	240	
ttgtttcttaa cattgtttca gagactccctc agacgcggcc tttgggtctt tcttaaagaa	300	
agatcttcgcg attttcgtt tgataacaaa ggaancactt tcagctgcga aaaaaaaaaanc	360	
accagtgttgg atggaaaataa cattattgtt gaaatgttccg atnataaccc accanattna	420	
aaaaaaaaaaatggcccaattt tccggaaaatn tggatcttaa gaataatctc ctggaaaacan	480	
aattataaaa cgtggaaaacc cggctncnt catttacnc	519	
<210> 19		
<211> 353		
<212> DNA		
<213> Zea mays		
<220>		
<221> misc_feature		
<222> (1)...(353)		
<223> n = A,T,C or G		
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ctcaaggcat ggttggagga gcagactctg ttccacttctt actccggcgtt gattttctgtt	60	
ggctatgtat ctcgtcgactt cgcancggc ggagggtggg gtggggtaac agtgaagctgt	120	
gtggactttt cccatgtggc cgagggtgtt ggggtgtatt tgaccacaac ttccctggcgg	180	
agctctgtctt gctgtatcaag ttccgttttt tgacattttt ccaganactt cttagacggc	240	
acgtttttgg tccttccttaa aaaaagatc cttgcacnttt ttgattttat tacnaaggaa	300	
acatttttca cttgcnnaaa aaaaaggccc ntgaggatataaaaatataac ntt	353	
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<211> 3416		
<212> DNA		
<213> Zea mays		
<220>		
<221> CDS		
<222> (72)...(407)		
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gtccccatatac c atg ccc gac ctc cac ccc ccc gag cac caa gtc gcc ggt	110	
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly		
1	5	10
cac cgc gcc tcc gcc agc aag ctg ggc cca ctc atc gac gac tct ggc	158	
His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly		
15	20	25
ctc ttc tac aag ccg ctc cag gcc gac cgt ggg gag cac gag gtc	206	
Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val		
30	35	40

20607070829007

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cagtcattc taatggaaag tcaggcttc ttgaaaaggt cgcaagctca cacttggttt	2787
gctctatagc actttctgcg aaaagtggga atctttctt aactgaattha atgttagaaat	2847
ggagccaaac aagtttatgt tttatggca cttcaagagt tgacaaaagg ttaagttctg	2907
agctccagaatc tcagaatgg agagttctt ctgtagctaa tgaatgtagc atagaggttc	2967
ctgggtttt aaatgttcaa aggcttcagc agttgtctt caccctggctt actctaaataa	3027
aaggaaacttctgtgtactt ctgttctgtt gatggatataatgaaaatattctgtga	3087
ggaagacttc gcaaggagat gtgggttctgtt cactttagtgc accgttgcg tttatggaga	3147
cgtgtatggaa gacggagaca agccagcgttataatgttgc agagatgtt ggttctgtga	3207
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gatgtacatc acttcactaa tcatgaaatc tgtagaaggc gaaactacta gccatataatg	3327
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tgaatttca aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa	3416

<210> 21
<211> 111
<212> PRT
<213> Zea mays

<400> 21
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
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Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr
20 25 30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
85 90 95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
100 105 110

<210> 22
<211> 1448
<212> DNA
<213> Parthenium argentatum

<220>
<221> CDS
<222> (52)...(1020)

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Met Leu
1

cca gct cca gct gtt cct aat ggc acg ggt gct ccg ctt aag gac gaa	105
Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu	
5 10 15	

cct tcc aac ccc gat cag gcg cac cag ctc gac gag cgc gtt caa	153
Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln	
20 25 30	

2060707-46824007

cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys 35 40 45 50	201
gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp 55 60 65	249
gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser 70 75 80	297
gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys 85 90 95	345
acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys 100 105 110	393
gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly 115 120 125 130	441
acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys 135 140 145	489
atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe 150 155 160	537
tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tgg Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser 165 170 175	585
aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac cgg Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro 180 185 190	633
agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly 195 200 205 210	681
ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys 215 220 225	729
ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu 230 235 240	777
cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg 245 250 255	825
ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile	873

260

265

270

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tgg aat gac atc aac gag gaa tgg gtc gaa cga ggc gag ggc gag ggc      921
Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly
275           280           285           290

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atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg 969
Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala
295           300           305

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ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc      1017
Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe
310          315          320

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taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt 1070
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cgatattgtat acgtccatcc ctttccctt cccttcattt ccaatgttcag tctatccac
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tctgggttttgg ttatgggttttggccaaatctt tggccggatctt tgatggccgtat
ttctttgtataatccataaa gaaatggatgg tggcttgcgttcc attataatccaa cactttgtat
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa

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<210> 23
<211> 322
<212> PRT
<213> *Parthenium argentatum*

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<400> 23
Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys
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Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg
      20          25          30
Val Glu His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg
      35          40          45
Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu
      50          55          60
Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr
      65          70          75          80
Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn
      85          90          95
Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp
      100         105         110
Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp
      115         120         125
Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu
      130         135         140
Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr
      145         150         155         160
Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly
      165         170         175
Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser
      180         185         190
Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser
      195         200         205

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Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu
 210 215 220
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp
 225 230 235 240
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile
 245 250 255
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln
 260 265 270
 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly
 275 280 285
 Glu Gly Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val
 290 295 300
 Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala
 305 310 315 320
 Ser Phe

<210> 24
 <211> 2270
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (3)...(953)

<400> 24
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 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe
 1 5 10 15

ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga 95
 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly
 20 25 30

cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143
 His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys
 35 40 45

aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp
 50 55 60

gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp
 65 70 75

gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr
 80 85 90 95

tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa 335
 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu
 100 105 110

gag gaa ctg gcg aaa gcc aaa gag aaa ccc aag ttg aga aaa gac atg 383
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met

206010-4168224007

	115	120	125	
tac gaa aaa atg att cag ata gac ccc aac gca cca tcg gag gag gaa				431
Tyr Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu				
130	135	140		
cac cga ctg aag ggt gtg aca aaa ccg agg tac atg gtt tgg agg gag				479
His Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu				
145	150	155		
acg att tcg tcc acg gcc acg ttg ggc ttc ccg atc gag ggg atc aag				527
Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys				
160	165	170	175	
aaa agc gat gga aaa tcg agc aag gac ttc aag acg aca aag aac ccg				575
Lys Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg				
180	185	190		
gac cag gtg atc gaa gcg ttt cga gat ttc gtc gcc ggt ttc ccg cac				623
Asp Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His				
195	200	205		
gta atc ccc aag tac ata aac cga ctg aga gcg atc aga gac ata ctg				671
Val Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu				
210	215	220		
gtg aac tcc aag ttt ttc act acg cac gag gtg atc ggc agc tcg ctg				719
Val Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu				
225	230	235		
ctg ttc gtg cac gac aag aac gcc aac ata tgg ctt atc gac ttc				767
Leu Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe				
240	245	250	255	
gca aag acg ctc ata ctt ccg ccg gac atc ccg atc aac cac acg tcc				815
Ala Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser				
260	265	270		
gag tgg gtg gtc aac cac gag gac atc ctg atc ggt atc aac				863
Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn				
275	280	285		
aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc				911
Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro				
290	295	300		
gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga				953
Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr *				
305	310	315		
acggccgtcga tccccggccgg taccctgact cgctcgccga cccactcgcc ggtgtcattt				1013
gatcccacgcc acccaactcg tagtcttgcg aatcacgtga cccaccccggt tgacaatgtg				1073
tgataataat aatatgtctg gccaaataa ttccaaaaat tttttttaa attacactttt				1133
cgattttcga cgacaaacaa aatgacgacg ttcccgatc ctatctacty tagggctgt				1193
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caggattt gccatcgta taaaacaaat gatcttattt agatgttaaa aaataatataat				1313
tatataatata tacatcatcg cggtgttgc tgataatgc ctatataat atgtactata				1373
ttatatacat acgatattat aaaaatagta tattattata ttatattata ataataatata				1433

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ggttatgtgt gtttgtgtgg aaatccaata atataaaaata atatgttataa tttttaaaata 1493
cttgtagat aatggacta ctacgtgtga ttctcaaata atatataat attaatattt 1553
taaacgtaca tttttaaatca caaacgtata tgacgtgtgt atatattt attatataat 1613
aattactata ctgtgcgtgc gataacata taattttgtc cctaatacat caatcaatta 1673
tccactgag tgtcgtgtgg tttttatcc gttgtttat ttatccgtca tcaactaaattt 1733
actatttta ttatccat tttttttttt ttcaaaaac ttgtttttat aatcagctcc 1793
ctccactacc cttttcacaa ccccttgcgtc ccatgtatca agcaaaataat tttttttt 1853
aataacatc acgttccaa cgacaaataat aataacaata atagatccata tactttttt 1913
ttatccctc acgaaaaacga gaagtcctca ttcttttc cccgttacagt gtgtgtgtgt 1973
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gctgtatgtgt gtgtgtgaaa ttttttattttt 2033
aattatataat tattataatt tttttcttctt ttatccat tttttttt aacattttttt 2093
ttgtgtgtac agaatattta aataagactt gtaaaaagaaa cccttgcgttatttattttt 2153
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Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys
35 40 45
Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val
50 55 60
Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp
65 70 75 80
Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser
85 90 95
Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu
100 105 110
Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr
115 120 125
Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His
130 135 140
Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr
145 150 155 160
Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys
165 170 175
Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp
180 185 190
Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val
195 200 205
Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val
210 215 220
Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu
225 230 235 240
Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala
245 250 255
Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu
260 265 270
Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn
275 280 285
Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val

100602-010902

290	295	300										
Thr	Leu	Ile	Glu	Val	Thr	Ala	Pro	Ser	Glu	Val	Thr	
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Gln

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Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
35 40